What is claimed is:

1. An isolated nucleic acid molecule selected from the group consisting of:

a) a nucleic acid molecule comprising a nucleotide sequence which is at least 60% identical to the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:3;

b) a nucleic acid molecule comprising a fragment of at least 300 nucleotides of the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:3;

c) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2;

d) a nucleic acid molecule which encodes a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2; and

e) a nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the nucleic acid molecule hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3, or a complement thereof, under stringent conditions.

2. The isolated nucleic acid molecule of claim 1, which is selected from the group consisting of:

a) a nucleic acid comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, and

b) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2.

3. The nucleic acid molecule of claim 1 further comprising vector nucleic acid sequences.

4. The nucleic acid molecule of claim 1 further comprising nucleic acid sequences encoding a heterologous polypeptide.

5. A host cell which contains the nucleic acid molecule of claim 1.

6. The host cell of claim 5 which is a mammalian host cell.

7. A non-human mammalian host cell containing the nucleic acid molecule of claim 1.

8. An isolated polypeptide selected from the group consisting of:

a) a polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 60% identical to a nucleic acid comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, or a complement thereof;

b) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3, or a complement thereof under stringent conditions; and

c) a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2.

9. The isolated polypeptide of claim 8 comprising the amino acid sequence of SEQ ID NO:2.

10. The polypeptide of claim 8 further comprising heterologous amino acid sequences.

11. An antibody which selectively binds to a polypeptide of claim 8.

12. A method for producing a polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2;

b) a polypeptide comprising a fragment of the amino acid sequence of SEQ ID NO:2, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2; and

c) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3;

comprising culturing the host cell of claim 5 under conditions in which the nucleic acid molecule is expressed.

13. A method for detecting the presence of a polypeptide of claim 8 in a sample, comprising:

a) contacting the sample with a compound which selectively binds to a polypeptide of claim 8; and

b) determining whether the compound binds to the polypeptide in the sample.

14. The method of claim 13, wherein the compound which binds to the polypeptide is an antibody.

15. A kit comprising a compound which selectively binds to a polypeptide of claim 8 and instructions for use.

16. A method for detecting the presence of a nucleic acid molecule of claim 1 in a sample, comprising the steps of:

a) contacting the sample with a nucleic acid probe or primer which selectively hybridizes to the nucleic acid molecule; and

b) determining whether the nucleic acid probe or primer binds to a nucleic acid molecule in the sample.

17. The method of claim 16, wherein the sample comprises mRNA molecules and is contacted with a nucleic acid probe.

18. A kit comprising a compound which selectively hybridizes to a nucleic acid molecule of claim 1 and instructions for use.

19. A method for identifying a compound which binds to a polypeptide of claim 8 comprising the steps of:

a) contacting a polypeptide, or a cell expressing a polypeptide of claim 8 with a test compound; and

b) determining whether the polypeptide binds to the test compound.

20. The method of claim 19, wherein the binding of the test compound to the polypeptide is detected by a method selected from the group consisting of:

a) detection of binding by direct detecting of test compound/polypeptide binding;

b) detection of binding using a competition binding assay;

c) detection of binding using an assay for 43238-mediated signal transduction..

21. A method for modulating the activity of a polypeptide of claim 8 comprising contacting a polypeptide or a cell expressing a polypeptide of claim 8 with a compound which binds to the polypeptide in a sufficient concentration to modulate the activity of the polypeptide.

22. A method for identifying a compound which modulates the activity of a polypeptide of claim 8, comprising:

a) contacting a polypeptide of claim 8 with a test compound; and

b) determining the effect of the test compound on the activity of the polypeptide to thereby identify a compound which modulates the activity of the polypeptide.

23. A method of identifying a nucleic acid molecule associated with a metabolic disorder comprising:

a) contacting a sample comprising nucleic acid molecules with a hybridization probe comprising at least 25 contiguous nucleotides of SEQ ID NO:1 or 3; and

b) detecting the presence of a nucleic acid molecule in said sample that hybridizes to said probe, thereby identifying a nucleic acid molecule associated with a metabolic disorder.

24. The method of claim 23, wherein said hybridization probe is detectably labeled.

25. The method of claim 23, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis and southern blotting prior to contacting with said hybridization probe.

26. The method of claim 23, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis and northern blotting prior to contacting with said hybridization probe.

27. The method of claim 23, wherein said detecting is by *in situ* hybridization.

28. A method of identifying a nucleic acid associated with a metabolic disorder comprising:

a) contacting a sample comprising nucleic acid molecules with a first and a second amplification primer, said first primer comprising at least 25 contiguous nucleotides of SEQ ID NO:1 or 3 and said second primer comprising at least 25 contiguous nucleotides from the complement of SEQ ID NO:1 or 3;

b) incubating said sample under conditions that allow nucleic acid amplification; and

c) detecting the presence of a nucleic acid molecule in said sample that is amplified, thereby identifying a nucleic acid molecule associated with a metabolic disorder.

29. The method of claim 6, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis after said incubation step.

30. The method of any one of claims 23 or 28, wherein said method is used to detect mRNA in said sample.

31. The method of any one of claims 23 or 28, wherein said method is used to detect genomic DNA in said sample.

32. A method of identifying a polypeptide associated with a metabolic disorder comprising:

a) contacting a sample comprising polypeptides with a 57242 binding substance; and

b) detecting the presence of a polypeptide in said sample that binds to said 57242 binding substance, thereby identifying a polypeptide associated with a metabolic disorder.

33. The method of claim 32, wherein said binding substance is an antibody.

34. The method of claim 32, wherein said binding substance is detectably labeled.

35. A method of identifying a subject having a metabolic disorder, or at risk for developing a metabolic disorder comprising:

a) contacting a sample obtained from said subject comprising nucleic acid molecules with a hybridization probe comprising at least 25 contiguous nucleotides of SEQ ID NO:1 or 3; and

b) detecting the presence of a nucleic acid molecule in said sample that hybridizes to said probe, thereby identifying a subject having a metabolic disorder, or at risk for developing a metabolic disorder.

36. The method of claim 35, wherein said hybridization probe is detectably labeled.

37. The method of claim 35, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis and southern blotting prior to contacting with said hybridization probe.

38. The method of claim 35, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis and northern blotting prior to contacting with said hybridization probe.

39. The method of claim 35, wherein said detecting is by *in situ* hybridization.

40. A method of identifying a subject having a metabolic disorder, or at risk for developing a metabolic disorder comprising:

a) contacting a sample obtained from said subject comprising nucleic acid molecules with a first and a second amplification primer, said first primer comprising at least 25 contiguous nucleotides of SEQ ID NO:1 or 3 and said second primer comprising at least 25 contiguous nucleotides from the complement of SEQ ID NO:1 or 3;

b) incubating said sample under conditions that allow nucleic acid amplification; and

c) detecting the presence of a nucleic acid molecule in said sample that is amplified, thereby identifying a subject having a metabolic disorder, or at risk for developing a metabolic disorder.

41. The method of claim 40, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis after said incubation step.

42. The method of any one of claims 35 or 40, wherein said method is used to detect mRNA in said sample.

43. The method of any one of claims 35 or 40, wherein said method is used to detect genomic DNA in said sample.

44. A method of identifying a subject having a metabolic disorder, or at risk for developing a metabolic disorder comprising:

a) contacting a sample obtained from said subject comprising polypeptides with a 57242 binding substance; and

b) detecting the presence of a polypeptide in said sample that binds to said 57242 binding substance, thereby identifying a subject having a metabolic disorder, or at risk for developing a metabolic disorder.

45. The method of claim 44, wherein said binding substance is an antibody.

46. The method of claim 44, wherein said binding substance is detectably labeled.

47. A method for identifying a compound capable of treating a metabolic disorder characterized by aberrant 57242 nucleic acid expression or 57242 polypeptide activity comprising assaying the ability of the compound to modulate 57242 nucleic acid expression or 57242 polypeptide activity, thereby identifying a compound capable of treating a metabolic disorder characterized by aberrant 57242 nucleic acid expression or 57242 polypeptide activity.

48. The method of claim 47, wherein the metabolic disorder is a disorder associated with aberrant lipogenesis.

49. The method of claim 47, wherein the disorder a disorder associated with aberrant lipolysis.

50. The method of claim 47, wherein the disorder is obesity.

51. The method of claim 47, wherein the disorder is diabetes.

52. The method of claim 47, wherein the ability of the compound to modulate the activity of the 57242 polypeptide is determined by detecting the induction of an intracellular second messenger.

53. A method for treating a subject having a metabolic disorder characterized by aberrant 57242 polypeptide activity or aberrant 57242 nucleic acid expression comprising administering to the subject a 57242 modulator, thereby treating said subject having a metabolic disorder.

54. The method of claim 53, wherein the 57242 modulator is a small molecule.

55. The method of claim 53, wherein the metabolic disorder is a disorder associated with aberrant lipogenesis.

56. The method of claim 53, wherein the disorder is a disorder associated with aberrant lipolysis.

57. The method of claim 53, wherein the metabolic disorder is obesity.

58. The method of claim 53, wherein the metabolic disorder is diabetes.

59. The method of claim 53, wherein said 57242 modulator is administered in a pharmaceutically acceptable formulation.

60. The method of claim 53, wherein said 57242 modulator is administered using a gene therapy vector.

61. The method of 53, wherein the 57242 modulator is capable of modulating 57242 polypeptide activity.

62. The method of claim 53, wherein the 57242 modulator is an anti-57242 antibody.

63. The method of claim 53, wherein the 57242 modulator is a 57242 polypeptide comprising the amino acid sequence of SEQ ID NO:2, or a fragment thereof.

64. The method of claim 53, wherein the 57242 modulator is a 57242 polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2.

65. The method of claim 53, wherein the 57242 modulator is an isolated naturally occurring allelic variant of a polypeptide consisting of the amino acid sequence of SEQ ID NO:2, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 or 3 under stringent conditions comprising 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C.

66. The method of claim 53, wherein the 57242 modulator is capable of modulating 57242 nucleic acid expression.

67. The method of claim 66, wherein the 57242 modulator is an antisense 57242 nucleic acid molecule.

68. The method of claim 66, wherein the 57242 modulator is a ribozyme.

69. The method of claim 66, wherein the 57242 modulator comprises the nucleotide sequence of SEQ ID NO:1 or 3, or a fragment thereof.

70. The method of claim 66, wherein the 57242 modulator comprises a nucleic acid molecule encoding a polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2.

71. The method of claim 66, wherein the 57242 modulator comprises a nucleic acid molecule encoding a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 or 3 under stringent conditions comprising 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C.

72. A method for identifying a compound capable of modulating an adipocyte activity comprising:

a) contacting an adipocyte with a test compound; and

b) assaying the ability of the test compound to modulate the expression of a 57242 nucleic acid or the activity of a 57242 polypeptide;

thereby identifying a compound capable of modulating an adipocyte activity.

73. The method of claim 72, wherein said adipocyte activity is hyperplastic growth.

74. The method of claim 72, wherein said adipocyte activity is hypertrophic growth.

75. The method of claim 72, wherein said adipocyte activity is lipogenesis.

76. A method for modulating an adipocyte activity comprising contacting an adipocyte with a 57242 modulator, thereby modulating said adipocyte activity.

77. The method of claim 76, wherein the 57242 modulator is a small molecule.

78. The method of claim 76, wherein said adipocyte activity is hyperplastic growth.

79. The method of claim 76, wherein said adipocyte activity is hypertrophic growth.

80. The method of claim 76, wherein said adipocyte activity is lipogenesis.

81. The method of claim 76, wherein the 57242 modulator is capable of modulating 57242 polypeptide activity.

82. The method of claim 81, wherein the 57242 modulator is an anti-57242 antibody.

83. The method of claim 59, wherein the 57242 modulator is a 57242 polypeptide comprising the amino acid sequence of SEQ ID NO:2, or a fragment thereof.

84. The method of claim 81, wherein the 57242 modulator is a 57242 polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2.

85. The method of claim 81, wherein the 57242 modulator is an isolated naturally occurring allelic variant of a polypeptide consisting of the amino acid sequence of SEQ ID

NO:2, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 or 3 under stringent conditions comprising 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C.

86. The method of claim 85, wherein the 57242 modulator is capable of modulating 57242 nucleic acid expression.

87. The method of claim 86, wherein the 57242 modulator is an antisense 57242 nucleic acid molecule.

88. The method of claim 86, wherein the 57242 modulator is a ribozyme.

89. The method of claim 86, wherein the 57242 modulator comprises the nucleotide sequence of SEQ ID NO:1 or 3, or a fragment thereof.

90. The method of claim 86, wherein the 57242 modulator comprises a nucleic acid molecule encoding a polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2.

91. The method of claim 86, wherein the 57242 modulator comprises a nucleic acid molecule encoding a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2 or 5, wherein the nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 or 3 under stringent conditions comprising 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C.

92. A method for treating a subject having a bone disorder characterized by aberrant 57242 polypeptide activity or aberrant 57242 nucleic acid expression comprising administering to the subject a 57242 modulator, thereby treating said subject having a bone disorder.

93. The method of claim 92, wherein the 57242 modulator is a small molecule.

94. The method of claim 92, wherein the disorder is a disorder associated with aberrant osteogenesis.

95. The method of claim 92, wherein the disorder is osteoporosis.

96. The method of claim 92, wherein the disorder is aberrant bone resorption.

97. The method of claim 92, wherein said 57242 modulator is administered in a pharmaceutically acceptable formulation.

98. The method of claim 92, wherein said 57242 modulator is administered using a gene therapy vector.

99. The method of claim 92, wherein the 57242 modulator is capable of modulating 57242 nucleic acid expression.

100. The method of claim 92, wherein the 57242 modulator is an antisense 57242 nucleic acid molecule.

101. The method of claim 92, wherein the 57242 modulator is a ribozyme.

102. The method of claim 92, wherein the 57242 modulator comprises the nucleotide sequence of SEQ ID NO:1 or 3, or a fragment thereof.

103. The method of claim 92, wherein the 57242 modulator comprises a nucleic acid molecule encoding a polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2.

104. The method of claim 92, wherein the 57242 modulator comprises a nucleic acid molecule encoding a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 or 3 under stringent conditions comprising 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C.